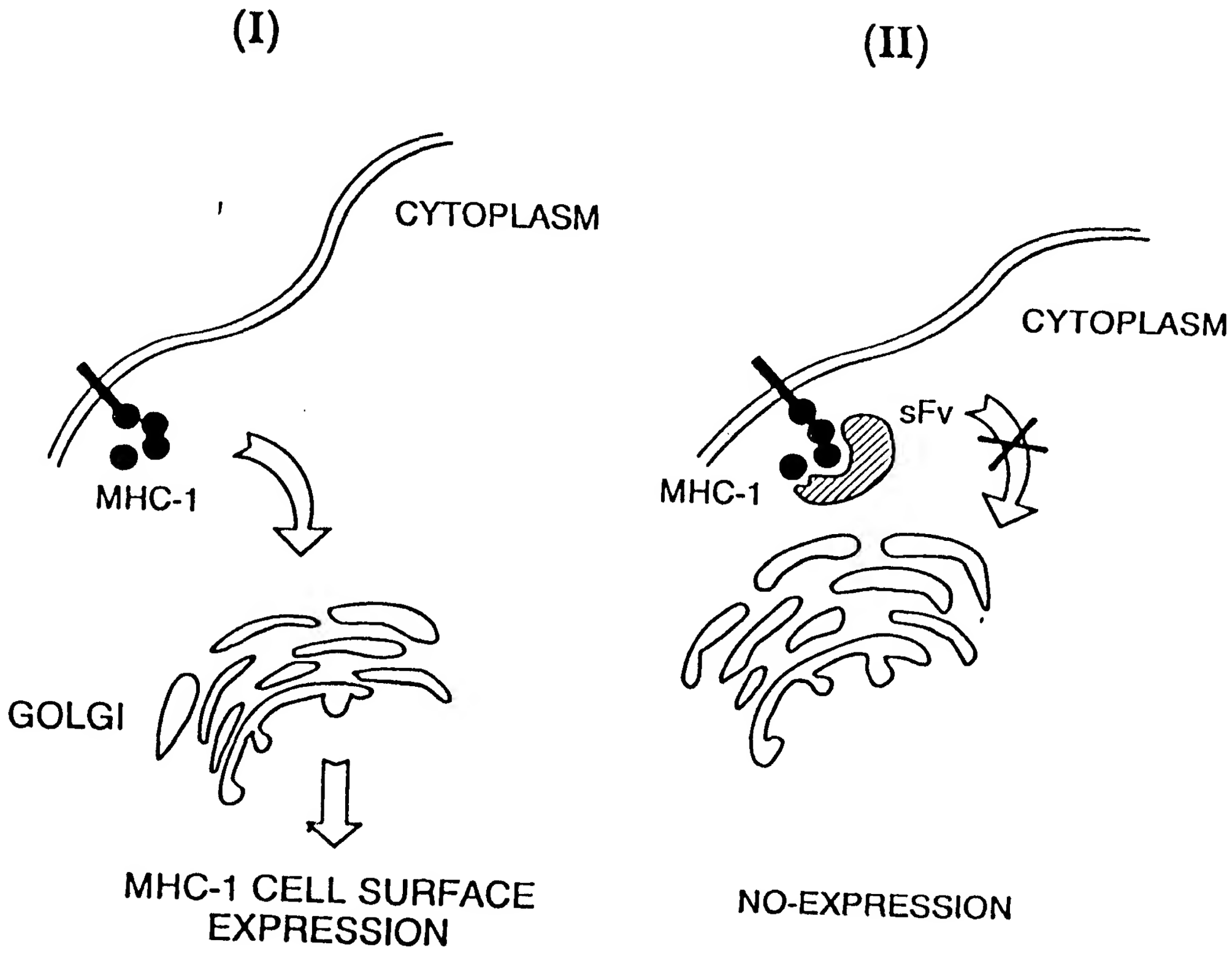

FIGURE 1

0952727 .031000

C1 (1f): |>u 1>+++++ 5ksfv (837 bases)+++++>u 837>|

```
    1                          21                                  41
    ATG GAA CAT CTG TGG TTC TTC CTT CTC CTG GTG GCA GCT CCC AGA
1:  met glu his leu trp phe phe leu leu leu val ala ala pro arg

                          61                                  81
    TGG GTC CTG TCC CAG GTG CAA CTG CAG CAG TCA GGG GCT GAG CTG
1:  trp val leu ser gln val gln leu gln gln ser gly ala glu leu

                  101                                 121
    GCA AGA CCT GGG GCT TCA GTG AAG TTG TCC TGC AAG GCT TCT GGC
1:  ala arg pro gly ala ser val lys leu ser cys lys ala ser gly

          141                         161
    TAC ACC TTT ACT AGT CAC TGG ATG CAG TGG GTG AGA CAG AGG CCT
1:  tyr thr phe thr ser his trp met gln trp val arg gln arg pro

    181                         201                                 221
    GGA CAG GGT CTG GAA TGG ATT GGG ACT ATT TAT CCT GGA GAT GGT
1:  gly gln gly leu glu trp ile gly thr ile tyr pro gly asp gly

                          241                                 261
    GAT ACT AGG TAC ACT CAG AAT TTC AAG GGC AAG GCC ACA TTG ACT
1:  asp thr arg tyr thr gln asn phe lys gly lys ala thr leu thr

                  281                                 301
    GCA GAT AAG TCC TCC ACC ACA GCC TAC TTA CAC CTC AGC AGC TTG
1:  ala asp lys ser ser thr thr ala tyr leu his leu ser ser leu

          321                         341
    TCA TCT GAA GAC TCT GCG GTC TAT TAT TGT GCA AGA GAT GAG ATT
1:  ser ser glu asp ser ala val tyr tyr cys ala arg asp glu ile

    361                         381                                 401
    ACT ACG GTT GTA CCC CGG GGG TTT GCT TAC TGG GGC CAA GGG ACC
1:  thr thr val val pro arg gly phe ala tyr trp gly gln gly thr

                          421                                 441
    TCG GTC ACC GTC TCC TCA GGT GGC GGT GGC TCG GGC GGT GGT GGC
1:  ser val thr val ser ser gly gly gly gly ser gly gly gly gly

                  461                                 481
    TCG GGT GGC GGC GGA TCT GAG CTC GTG CTC ACC CAA ACC CCA ACC
1:  ser gly gly gly gly ser glu leu val leu thr gln thr pro thr

          501                         521
    TCC CTG GCT NCC TCT CTG GGA GAC AGA GTC ACC ATC AGT TGC AGG
1:  ser leu ala --- ser leu gly asp arg val thr ile ser cys arg

    541                         561                                 581
    GCA AGT CAG GAC ATT AGC AGT TAT TTA AAC TGG TAT CAG CAG AAA
1:  ala ser gln asp ile ser ser tyr leu asn trp tyr gln gln lys

                          601                                 621
    CCA GAT GGA ACT ATT AAA CTC CTG ATC TAC TAC ACA TCA AGA TTA
```

FIGURE 2A

```
1: pro asp gly thr ile lys leu leu ile tyr tyr thr ser arg leu

                  641                                 661
   TAT TCA GGA GTC CCA CCA AGG TTC AGT GGC AGT GGG GCT GGA ACA
1: tyr ser gly val pro pro arg phe ser gly ser gly ala gly thr

         681                                 701
   GAT TAT TCT CTC ACC ATC AGC AAC CTG GAG CAA GAA GAT TTT GCC
1: asp tyr ser leu thr ile ser asn leu glu gln glu asp phe ala

   721                                 741                 761
   ACT TAC TTT TGC CAA CAG GGT AAT GTG ATT CCG TAC ACG TTC GGA
1: thr tyr phe cys gln gln gly asn val ile pro tyr thr phe gly

                     781                                 801
   GGG GGG ACC AAG CTG GAA ATG AAA CGG GCT GAT GCT GCA CCA ACT
1: gly gly thr lys leu glu met lys arg ala asp ala ala pro thr

                  821
   GTA AGC GAA AAG GAC GAG CTG TAA TAA
1: val ser glu lys asp glu leu *** ***
```

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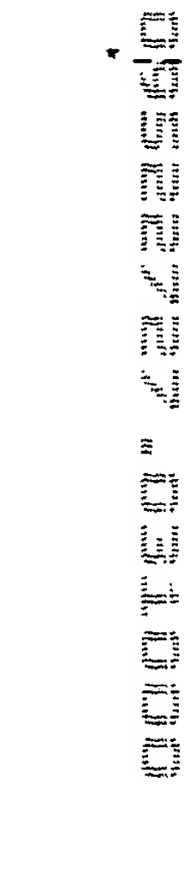
C1 (1f): |>u 1>+++++ mhc8sfv (837 bases)+++++>u 837>|

```
   1                              21                                  41
   ATG GAA CAT CTG TGG TTC TTC CTT CTC CTG GTG GCA GCT CCC AGA
1: met glu his leu trp phe phe leu leu leu val ala ala pro arg

                           61                                  81
   TGG GTC CTG TCC CAG GTG CAA CTG CAG CAG TCT GGG GCT GAG CTG
1: trp val leu ser gln val gln leu gln gln ser gly ala glu leu

                 101                                 121
   ACA AGA CCT GGG GCT TCA GTG AAG TTG TCC TGC AAG GCT TCT GGC
1: thr arg pro gly ala ser val lys leu ser cys lys ala ser gly

         141                                 161
   TAC ACC TTT ACT AGT CAC TGG ATG CAG TGG GTG AGA CAG AGG CCT
1: tyr thr phe thr ser his trp met gln trp val arg gln arg pro

   181                              201                                 221
   GGA CAG GGT CTG GAA TGG ATT GGG ACT ATT TAT CCT GGA GAT GGT
1: gly gln gly leu glu trp ile gly thr ile tyr pro gly asp gly

                           241                                 261
   GAT ACT AGG TAC ACT CAG AAT TTC AAG GGC AAG GCC ACA TTG ACT
1: asp thr arg tyr thr gln asn phe lys gly lys ala thr leu thr

                 281                                 301
   GCA GAT AAG TCC TCC ACC ACA GCC TAC TTA CAC CTC AGC AGC TTG
1: ala asp lys ser ser thr thr ala tyr leu his leu ser ser leu

         321                                 341
   TCA TCT GAA GAC TCT GCG GTC TAT TAT TGT GCA AGA GAT GAG ATT
1: ser ser glu asp ser ala val tyr tyr cys ala arg asp glu ile

   361                              381                                 401
   ACT ACG GTT GTA CCC CGG GGG TTT GCT TAC TGG GGC CAA GGG ACC
1: thr thr val val pro arg gly phe ala tyr trp gly gln gly thr

                           421                                 441
   TTG GTC ACC GTC TCC TCA GGT GGC GGT GGC TCG GGC GGT GGT GGG
1: leu val thr val ser ser gly gly gly gly ser gly gly gly gly

                 461                                 481
   TCG GGT GGC GGC GGA TCT GAG CTC GTG CTC ACC CAG TCT CCA TCC
1: ser gly gly gly gly ser glu leu val leu thr gln ser pro ser

         501                                 521
   AGT CTG TCT GCA TCC CTT GGA GAC ACA ATT ACC ATC ACT TGC CAT
1: ser leu ser ala ser leu gly asp thr ile thr ile thr cys his

   541                              561                                 581
   GCC AGT CAG AAC ATT AAT GTT TGG TTA AGT TGG TAC CAG CAG AAA
1: ala ser gln asn ile asn val trp leu ser trp tyr gln gln lys

                           601                                 621
   CCA GGA AAT ATT CCT CAA CTA TTG ATC TAT AAG GCT TCC AAC TTG
```

FIGURE 2B

```
1: pro gly asn ile pro gln leu leu ile tyr lys ala ser asn leu

                641                                661
   CAC ACA GGC GTC CCA TCA AGG TTT AGT GGC CGT GGA TCT GGA ACA
1: his thr gly val pro ser arg phe ser gly arg gly ser gly thr

        681                            701
   GGT TTC ACA TTA ACC ATC AGC AGC CTG CAG CCT GAA GAC ATT GGC
1: gly phe thr leu thr ile ser ser leu gln pro glu asp ile gly

   721                            741                            761
   ACT TAC TAC TGT CAA CAG GGT CAA AGT TAT CCT CTG ACG TTC GGT
1: thr tyr tyr cys gln gln gly gln ser tyr pro leu thr phe gly

                  781                            801
   GGA GGC ACC AAG CTG GAA ATC AAA CGG GCT GAT GCT GCA CCA ACT
1: gly gly thr lys leu glu ile lys arg ala asp ala ala pro thr

                821
   GTA AGC GAA AAG GAC GAG CTG TAA TAA
1: val ser glu lys asp glu leu *** ***
```



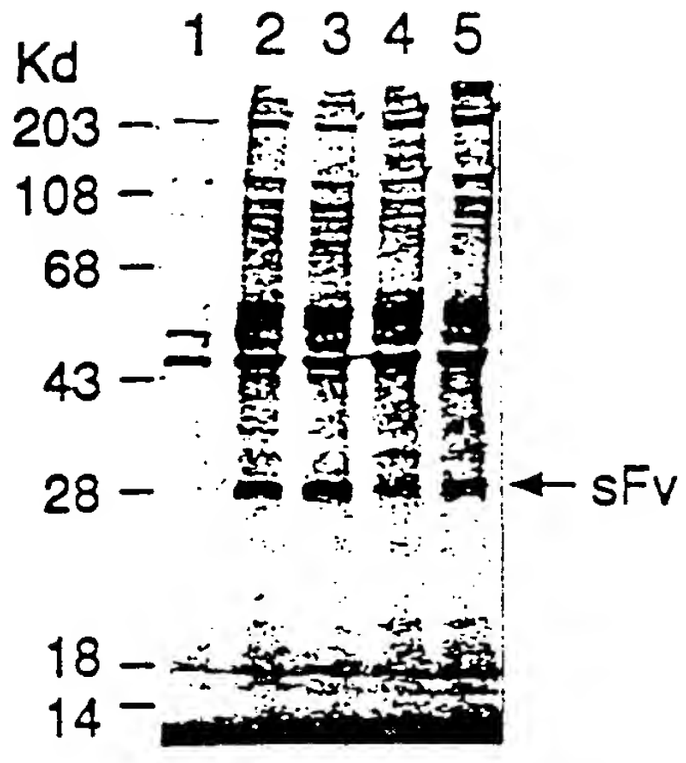


FIGURE 3

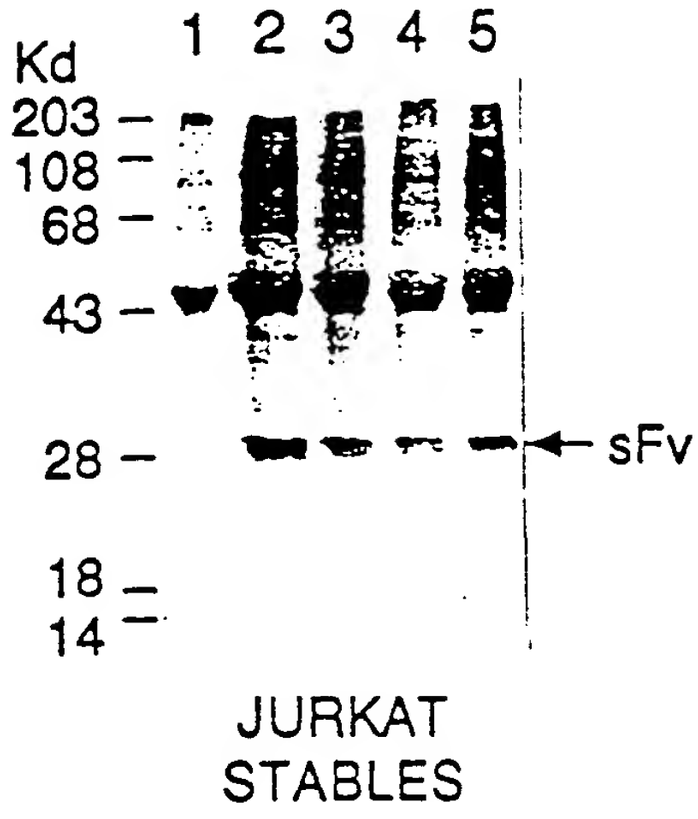


FIGURE 4

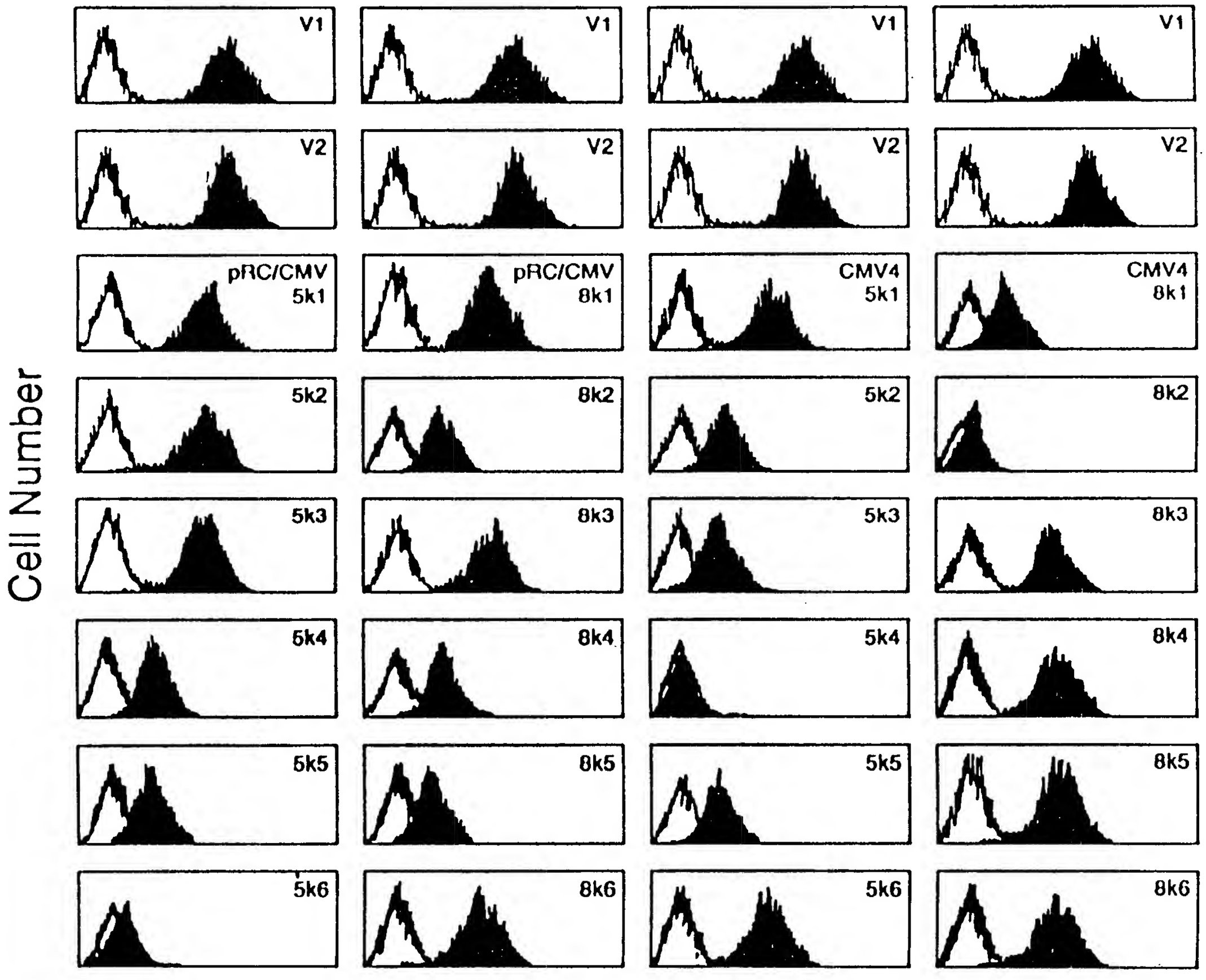


FIGURE 5

0952727 .03J.003

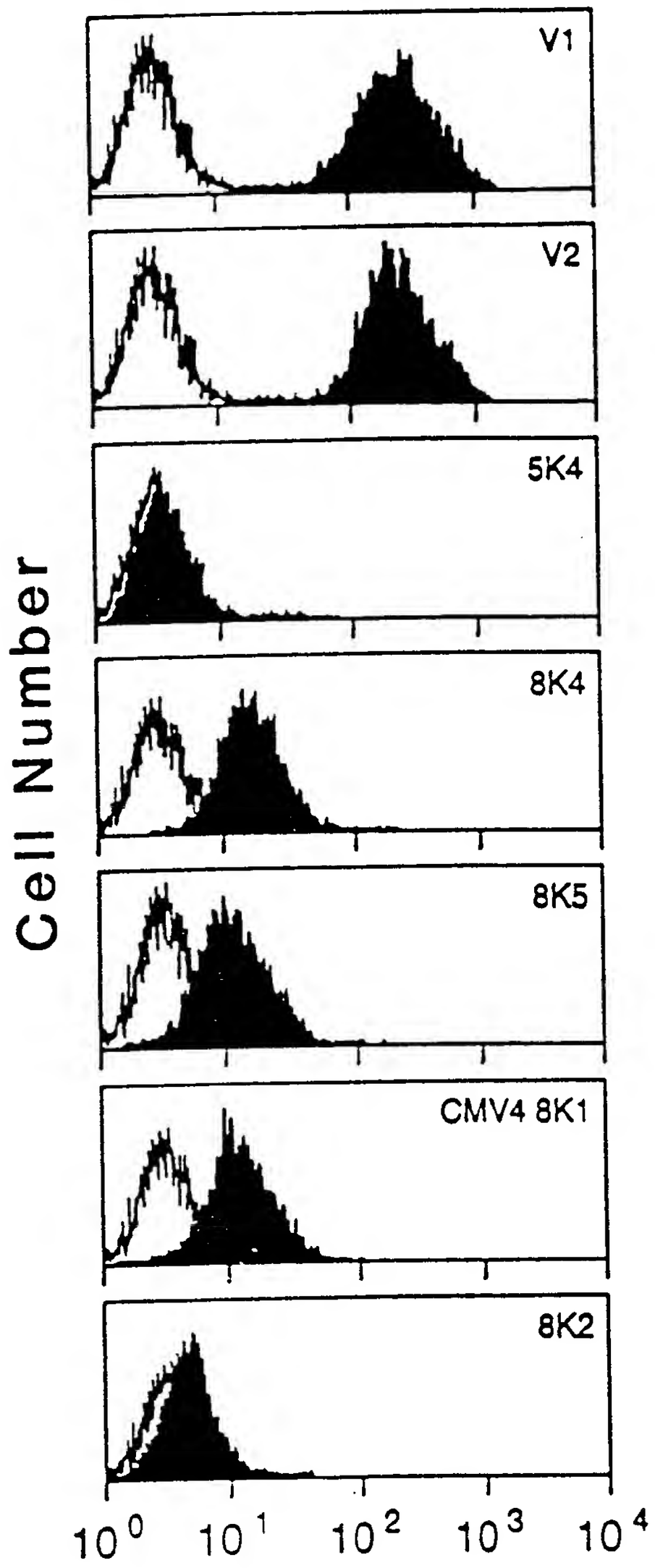

V1
V2
5K4
8K4
8K5
CMV4 8K1
8K2
Cell Number
10 0
10 1
10 2
10 3
10 4
Jurkat Stable Clones

FIGURE 6

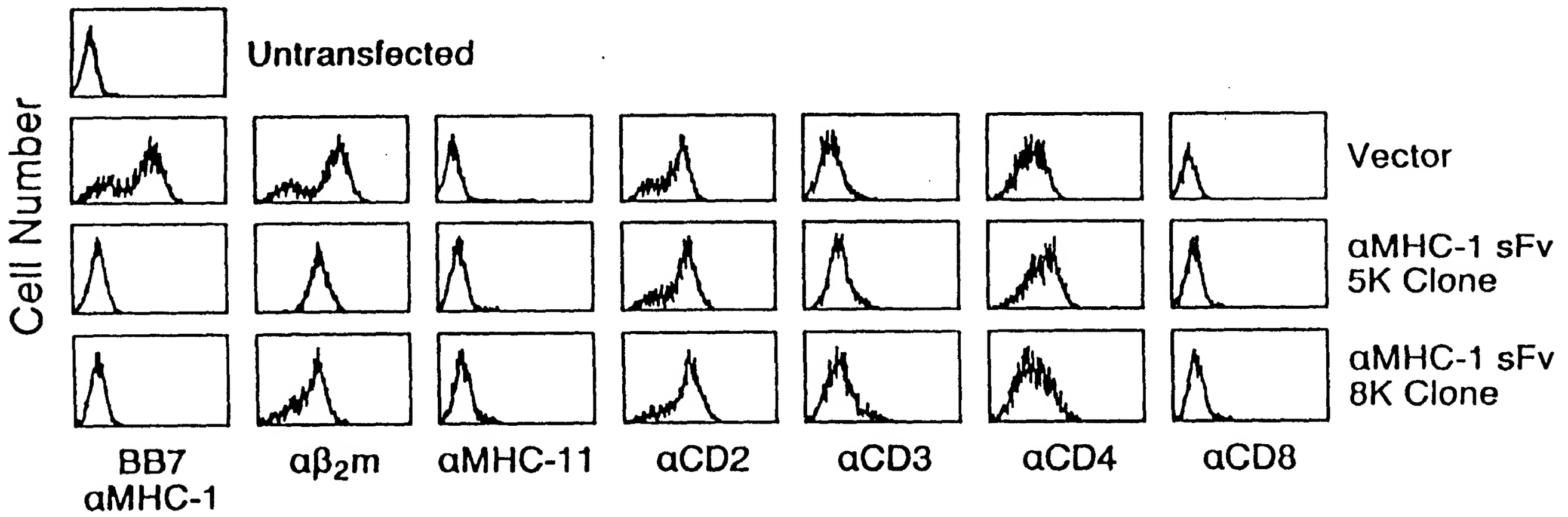


FIGURE 7

0362727 .03100